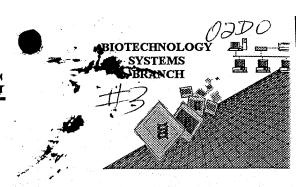# RAW SEQUENCE LISTING
## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/545,283_

Art Unit / Team No. : _OIPE_

Date Processed by STIC: _4/30/2000_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

# Raw Sequence Listing Error Summary

ERROR DETECTED    SUGGESTED CORRECTION      SERIAL NUMBER: 09/545,283

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
**(2) INFORMATION FOR SEQ ID NO:X:**
**(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**
**This sequence is intentionally skipped**

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
**<210> sequence id number**
**<400> sequence id number**
**000**

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
**Please explain source of genetic material in <220> to <223> section.**
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)    (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

*Does Not Comply*
*Corrected Diskette Needed*

```
 3 <110> APPLICANT: Boyle, Bryan J.
 4               Ford, John E.
 5               Mize, Nancy K.
 6               Tang, Y. Tom
 7               Tillinghast, John
 8               Sinku, Ankura
 9               Liu, Chenghua
10               Drmanac, Radoje T
11               Dickson, Mark C
12               Arterburn, Matthew C
14 <120> TITLE OF INVENTION: Methods and Materials Relating to Novel C-Type Lectin
15               Receptor-Like Polypeptides and Polynucleotides
17 <130> FILE REFERENCE: HYS-5
19 <140> CURRENT APPLICATION NUMBER: US/09/545,283
20 <141> CURRENT FILING DATE: 2000-04-07
22 <150> PRIOR APPLICATION NUMBER: 09/496,914
23 <151> PRIOR FILING DATE: 2000-02-03
25 <160> NUMBER OF SEQ ID NOS: 7
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 415
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <400> SEQUENCE: 1
35 cgcacacaca atggtgcctg aagaagagcc tcaagaccga gagaaaggac tctggtgggt 60
36 ccaggtgaag gtctggtcca tggcagtcgt atccatcttg ctcctcagtg tctgtttcac 120
37 tgtgagttct gtggtgcctc acaattttat gtatagcaaa actgtcaaga ggctgtccaa 180
38 gttacgagag tatcaacagt atcattcaag cctgacctgc gtcatggaag gaaaggacat 240
39 agaagattgg agctgctgcc caaccccttg gacttcattt cagtctagtt gctactttat 300
40 ttctactggg atgcaatctt ggactaagag tcaaaagaac tgttctgtga tggggctga 360
41 tctggtggtg atcaacacca gggaagaaca ggatttcatc attcagaatc tga    415
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 826
46 <212> TYPE: DNA
47 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 2
50 cgcacacaca atggtgcctg aagaagagcc tcaagaccga gagaaaggac tctggtgggt 60
51 ccaggtgaag gtctggtcca tggcagtcgt atccatcttg ctcctcagtg tctgtttcac 120
52 tgtgagttct gtggtgcctc acaattttat gtatagcaaa actgtcaaga ggctgtccaa 180
53 gttacgagag tatcaacagt atcattcaag cctgacctgc gtcatggaag gaaaggacat 240
54 agaagattgg agctgctgcc caaccccttg gacttcattt cagtctagtt gctactttat 300
55 ttctactggg atgcaatctt ggactaagag tcaaaagaac tgttctgtga tggggctga 360
56 tctggtggtg atcaacacca gggaagaaca ggatttcatc attcagaatc tgaaaagaaa 420
57 ttcttcttat tttctggggc tgtcagatcc aggggtcgg cgacattggc aatgggttga 480
58 ccagacacca tacaatgaaa atgtcacgtg agtatagaat gagattctgg cactcaggtg 540
59 aacccaataa ccttgatgag cgttgtgcga taataaattt ccgttcttca gaagaatggg 600
60 gctggaatga cattcactgt catgtacctc agaagtcaat ttgcaagatg aagaagatct 660
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*se iten 10 on Eva Summary Sheet*

**RAW SEQUENCE LISTING**          DATE: 05/02/2000
PATENT APPLICATION: **US/09/545,283**          TIME: 08:51:02

Input Set : **A:\C-type1.app**
Output Set: **N:\CRF3\050200\I545283.raw**

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61 acatataaat gaaatattct ccctggaaat gtgtttgggt tggcatccac cgttgtagaa 720
62 agctaaattg attttttaat ttatgtgtaa gttttgtaca aggaatgccc ctaaaatgtt 780
63 tcagcaggct gtcacctatt acacttatga tataatccat ttaaaa           826
66 <210> SEQ ID NO: 3
67 <211> LENGTH: 858
68 <212> TYPE: DNA
69 <213> ORGANISM: Homo sapiens
71 <220> FEATURE:
72 <221> NAME/KEY: CDS
73 <222> LOCATION: (43)..(747)
75 <400> SEQUENCE: 3
76 tgaacttaat tttgggtcga cccacgcgtc cgcgcacaca ca atg gtg cct gaa    54
77                                                 Met Val Pro Glu
78                                                  1
80 gaa gag cct caa gac cga gag aaa gga ctc tgg tgg ttc cag ttg aag   102
81 Glu Glu Pro Gln Asp Arg Glu Lys Gly Leu Trp Trp Phe Gln Leu Lys
82  5                10                  15                  20
84 gtc tgg tcc atg gca gtc gta tcc atc ttg ctc ctc agt gtc tgt ttc   150
85 Val Trp Ser Met Ala Val Val Ser Ile Leu Leu Leu Ser Val Cys Phe
86                  25                  30                  35
88 act gtg agt tct gtg gtg cct cac aat ttt atg tat agc aaa act gtc   198
89 Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr Ser Lys Thr Val
90                  40                  45                  50
92 aag agg ctg tcc aag tta cga gag tat caa cag tat cat tca agc ctg   246
93 Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr His Ser Ser Leu
94           55                  60                  65
96 acc tgc gtc atg gaa gga aag gac ata gaa gat tgg agc tgc tgc cca   294
97 Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp Ser Cys Cys Pro
98           70                  75                  80
100 acc cct tgg act tca ttt cag tct agt tgc tac ttt att tct act ggg  342
101 Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe Ile Ser Thr Gly
102  85                  90                  95                 100
104 atg caa tct tgg act aag agt caa aag aac tgt tct gtg atg ggg gct  390
105 Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser Val Met Gly Ala
106                 105                 110                 115
108 gat ctg gtg gtg atc aac acc acg gaa gaa cac gat ttc atc att cat  438
109 Asp Leu Val Val Ile Asn Thr Thr Glu Glu His Asp Phe Ile Ile His
110                 120                 125                 130
112 aat ctg aaa aga aat tct tct tat ttt ctg ggg ctg tca cat cca cgg  486
113 Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu Ser His Pro Arg
114          135                 140                 145
116 ggt cgg cga cat tgg caa tgg gtt gac cac aca cca tac aat gaa aat  534
117 Gly Arg Arg His Trp Gln Trp Val Asp His Thr Pro Tyr Asn Glu Asn
118  150                 155                 160
120 gtc aca ttc tgg cac tca ggt gaa ccc aat aac ctt gat gag cgt tgt  582
121 Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu Asp Glu Arg Cys
122 165                 170                 175                 180
124 gcg ata ata aat ttc cgc tct tca caa gaa tgg ggc tgg aat gac att  630
125 Ala Ile Ile Asn Phe Arg Ser Ser Gln Glu Trp Gly Trp Asn Asp Ile
```

```
                    RAW SEQUENCE LISTING              DATE: 05/02/2000
                    PATENT APPLICATION:  US/09/545,283    TIME: 08:51:02

                    Input Set : A:\C-type1.app
                    Output Set: N:\CRF3\050200\I545283.raw

126                      185                   190                   195
128 cac tgt cat gta cct cac aag tca att tgc gag atg aag aag atc tac    678
129 His Cys His Val Pro His Lys Ser Ile Cys Glu Met Lys Lys Ile Tyr
130              200                   205                   210
132 ata tac atg aaa tat tct ccc tgg aaa tgt gtt tgg gtt ggc atc cac    726
133 Ile Tyr Met Lys Tyr Ser Pro Trp Lys Cys Val Trp Val Gly Ile His
134              215                   220                   225
136 cgc tgt aga aag cta aat tga tttttttaatt tatgtgtaag atttgtacaa      777
137 Arg Cys Arg Lys Leu Asn
138        230                   235
140 agaatgcccc taaatgtttc agcaggctgt cacctattac acttatgata taatccattc 837
142 acacattcaa aaaaaaaaaa g                                            858
145 <210> SEQ ID NO: 4
146 <211> LENGTH: 234
147 <212> TYPE: PRT
148 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 4
151 Met Val Pro Glu Glu Pro Gln Asp Arg Glu Lys Gly Leu Trp Trp
152   1               5                  10                  15
153 Phe Gln Leu Lys Val Trp Ser Met Ala Val Val Ser Ile Leu Leu Leu
154            20                  25                  30
155 Ser Val Cys Phe Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr
156            35                  40                  45
157 Ser Lys Thr Val Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr
158       50                  55                  60
159 His Ser Ser Leu Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp
160   65                  70                  75                  80
161 Ser Cys Cys Pro Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe
162            85                  90                  95
163 Ile Ser Thr Gly Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser
164            100                 105                 110
165 Val Met Gly Ala Asp Leu Val Val Ile Asn Thr Thr Glu Glu His Asp
166       115                 120                 125
167 Phe Ile Ile His Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu
168       130                 135                 140
169 Ser His Pro Arg Gly Arg Arg His Trp Gln Trp Val Asp His Thr Pro
170 145                 150                 155                 160
171 Tyr Asn Glu Asn Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu
172            165                 170                 175
173 Asp Glu Arg Cys Ala Ile Ile Asn Phe Arg Ser Ser Gln Glu Trp Gly
174            180                 185                 190
175 Trp Asn Asp Ile His Cys His Val Pro His Lys Ser Ile Cys Glu Met
176       195                 200                 205
177 Lys Lys Ile Tyr Ile Tyr Met Lys Tyr Ser Pro Trp Lys Cys Val Trp
178       210                 215                 220
179 Val Gly Ile His Arg Cys Arg Lys Leu Asn
180 225                 230
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 14
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186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 5
190 Trp Asn Asp Ile His Cys His Val Pro His Lys Ser Ile Cys
191   1               5                 10
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195 <211> LENGTH: 193
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 6
200 Val Pro His Asn Phe Met Tyr Ser Lys Thr Val Lys Arg Leu Ser Lys
201   1               5                 10                  15
203 Leu Arg Glu Tyr Gln Gln Tyr His Ser Ser Leu Thr Cys Val Met Glu
204          20                  25                  30
206 Gly Lys Asp Ile Glu Asp Trp Ser Cys Cys Pro Thr Pro Trp Thr Ser
207          35                  40                  45
209 Phe Gln Ser Ser Cys Tyr Phe Ile Ser Thr Gly Met Gln Ser Trp Thr
210          50                  55                  60
212 Lys Ser Gln Lys Asn Cys Ser Val Met Gly Ala Asp Leu Val Val Ile
213   65                  70                  75                  80
215 Asn Thr Thr Glu Glu His Asp Phe Ile Ile His Asn Leu Lys Arg Asn
216                  85                  90                  95
218 Ser Ser Tyr Phe Leu Gly Leu Ser His Pro Arg Gly Arg Arg His Trp
219          100                 105                 110
221 Gln Trp Val Asp His Thr Pro Tyr Asn Glu Asn Val Thr Phe Trp His
222          115                 120                 125
224 Ser Gly Glu Pro Asn Asn Leu Asp Glu Arg Cys Ala Ile Ile Asn Phe
225          130                 135                 140
227 Arg Ser Ser Gln Glu Trp Gly Trp Asn Asp Ile His Cys His Val Pro
228 145                 150                 155                 160
230 His Lys Ser Ile Cys Glu Met Lys Lys Ile Tyr Ile Tyr Met Lys Tyr
231                 165                 170                 175
233 Ser Pro Trp Lys Cys Val Trp Val Gly Ile His Arg Cys Arg Lys Leu
234          180                 185                 190
236 Asn
240 <210> SEQ ID NO: 7
241 <211> LENGTH: 18
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 7
246 Cys Tyr Phe Ile Ser Thr Gly Met Gln Ser Trp Thr Lys Ser Gln Lys
247   1               5                 10                  15
249 Asn Cys
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**VERIFICATION SUMMARY**
PATENT APPLICATION: **US/09/545,283**

DATE: 05/02/2000
TIME: 08:51:03

Input Set : **A:\C-type1.app**
Output Set: **N:\CRF3\050200\I545283.raw**

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L:19  M:270 C: Current Application Number differs, Replaced Current Application Number
L:41  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:41  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:41  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:41  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:41  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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